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Complete Genome Sequence of the Marine Cellulose- and Xylan-Degrading Bacterium Glaciecola sp. Strain 4H-3-7+YE5

B. Klippel, A. Lochner, D. Bruce, K. Davenport, C. Detter, L. Goodwin, J. Han, S. Han, L. Hauser, M. Land, N. Mikhailova, M. Nolan, L. Pennacchio, S. Pitluck, R. Tapia, T. Woyke, S. Wiebusch, A. Basner, F. Abe, K. Horikoshi, M. Keller, G. Antranikian

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[1]Institute of Technical Microbiology, Hamburg University of Technology, Hamburg, Germany
[2]Oak Ridge National Laboratory, Oak Ridge, Tennessee 37831, USA
[3]Los Alamos National Laboratory, Los Alamos, New Mexico 87545, USA
[4]DOE Joint Genome Institute, Walnut Creek, California 94598, USA
[5]Extremobiosphere Research Center (XBR), Japan Agency for Marine-Earth Science and Technology (JAMSTEC), Yokosuka, Japan

*Corresponding author. Institute of Technical Microbiology, Hamburg University of Technology, Kasernenstr. 12, D-21073 Hamburg, Germany. Phone: +49 40 42878 3117. Fax: +49 40 42878 2582. Email: antranikian@tuhh.de

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Abstract

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In order to gain insight into the complete gene repertoire of *Glaciecola* sp. 4H-3-7+YE-5, the genome was sequenced at the DOE Joint genome Institute (JGI) using a combination of Illumina (2) and 454 technologies (10). To this end, we constructed and sequenced an Illumina GAii shotgun library which generated 50,060,436 reads totaling 3,804 Mb, a 454 Titanium standard library which generated 233,681 reads and three paired end 454 libraries with an average insert sizes of 10.0 kb, 5.4 kb, and 5.9 kb which generated 272,557 reads totaling 164.4 Mb of 454 data. All general aspects of library construction and sequencing can be found at http://www.jgi.doe.gov/. The initial draft assembly contained 55 contigs in 2 scaffolds. The 454 Titanium standard data and the 454 paired end data were assembled together with Newbler, version 2.3 while the Illumina sequencing data was assembled with VELVET, version 0.7.63 (16). Newbler and Illumina VELVET consensus data as well as read pairs in the 454 paired end library were integrated using parallel phrap, version SPS - 4.24 (High Performance Software, LLC). The software Consed (5-7) was used in the following finishing process. Illumina data was used to increase consensus quality using the software Polisher (Alla Lapidus, unpublished). Mis-assemblies were corrected using gapResolution (Cliff Han, unpublished), Dupfinisher (9), or sequencing cloned bridging PCR fragments. Gaps between contigs were closed by editing in Consed, by PCR and by Bubble PCR (J-F Cheng, unpublished) primer walks. A total of 209 additional reactions were necessary to close gaps and to raise the quality of the finished sequence. The total size of the genome is 5,393,591 bp and the final assembly is based on 137.8 Mb of 454 draft

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The genome of *Glaciecola* sp. 4H-3-7+YE-5 is contained within one large chromosome (5,052,309 bp) and one plasmid (pGLAAG01, 341,282 bp). The complete genome has a total G+C content of 44% and comprises 4,548 predicted protein-encoding genes.

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Nucleotide sequence accession number. The complete chromosome and plasmid sequences of *Glaciecola* sp. 4H-3-7+YE-5 have been deposited in GenBank under accession numbers CP002526 and CP002527.

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